

Nucleotide and Amino Acid Sequence of AIM-I

-51	GGCACGAGCGGCTGCCTGGCTGACTTACAGCAGTCAGACTCTGACAGGTTCA	8
-16	CCGTGCTCGCCGACGGACCGACTGAATGTCGTCAGTCTGAGACTGTCCAAGTACCGATAC	3
	M A M	
9	ATGGAGGTCCAGGGGGACCCAGCCTGGGACAGACCTGCGTGCTGATCGTGATCTTCACA	68
4	TACCTCCAGGTCCCCCTGGGTCGGACCTGTCTGGACGCACGACTAGCACTAGAAGTGT	23
	M E V Q G G P S L G Q T C V L I V I F T	
69	GTGCTCCTGCAGTCTCTCTGTGTGGCTGTAACCTACGTGTACTTTACCAACGAGCTGAAG	128
24	CACGAGGACGTCAGAGAGACACACCGACATTGAATGCACATGAAATGGTTGCTCGACTTC	43
	V L L Q S L C V A V T Y V Y F T N E L K	
129	CAGATGCAGGACAAGTACTCCAAAAGTGGCATTGCTTGTTTCTTAAAAGAAGATGACAGT	188
44	GTCTACGTCCTGTTTCATGAGGTTTTACCGTAACGAACAAAGAATTTTCTTCTACTGTCA	63
	Q M Q D K Y S K S G I A C F L K E D D S	
189	TATTGGGACCCCAATGACGAAGAGAGTATGAACAGCCCCTGCTGGCAAGTCAAGTGGCAA	248
64	ATAACCCTGGGGTTACTGCTTCTCTCATACTTGTCTGGGGACGACCGTTCAAGTTCACCGTT	83
	Y W D P N D E E S M N S P C W Q V K W Q	
249	CTCCGTGCTGCTGTTAGAAAGATGATTTTGAGAACCTCTGAGGAAACCATTTCTACAGTT	308
84	GAGGCAGTCGAGCAATCTTTCTACTAAAACTCTTGAGACTCCTTTGGTAAAGATGTCAA	103
	L R Q L V R K M I L R T S E E T I S T V	
309	CAAGAAAAGCAACAAAATATTTCTCCCTAGTGAGAGAAAAGAGGTCCTCAGAGAGTAGCA	368
104	GTTCTTTTCGTTGTTTTATAAAGAGGGGATCACTCTCTTCTCCAGGAGTCTCTCATCGT	123
	Q E K Q Q N I S P L V R E R G P Q R V A	
369	GCTCACATAACTGGGACCAGAGGAAGAAGCAACACATTGTCTTCTCCAAACTCCAAGAAT	428
124	CGAGTGTATTGACCCTGGTCTCCTTCTCGTTGTGTAACAGAAGAGGTTTGAGGTTCTTA	143
	A H I T G T R G R S N T L S S P N S K N	
429	GAAAAGGCTCTGGGCCGCAAAATAAACTCCTGGGAATCATCAAGGAGTGGGCATTTCATTC	488
144	CTTTTCCGAGACCCGGCGTTTTATTTGAGGACCTTAGTAGTTCCTCACCCGTAAGTAAG	163
	E K A L G R K I N S W E S S R S G H S F	

FIG.1A

489	CTGAGCAACTTGCACTTGAGGAATGGTGAAGTGGTCATCCATGAAAAAGGGTTTTACTAC	548
	-+-----+-----+-----+-----+-----+-----+-----+-----	
164	GACTCGTTGAACGTGAAGTCTTACCCTTGACCAGTAGGTACTTTTTCCCAAATGATG	183
	L S N L H L R N G E L V I H E K G F Y Y	
549	ATCTATTCCCAACATACTTTTCGATTTTCAGGAGGAAATAAAAGAAAACACAAAGAACGAC	608
	-+-----+-----+-----+-----+-----+-----+-----+-----	
184	TAGATAAGGGTTTGTATGAAAGCTAAAGTCCTCTTTATTTTCTTTTGTGTTTCTTGCTG	203
	I Y S Q T Y F R F Q E E I K E N T K N D	
609	AAACAAATGGTCCAATATATTTACAAATACACAAGTTATCCTGACCCTATATTGTTGATG	668
	-+-----+-----+-----+-----+-----+-----+-----+-----	
204	TTTGTTTACCAGGTTATATAAATGTTTATGTGTTCAATAGGACTGGGATATAACAACACTAC	223
	K Q M V Q Y I Y K Y T S Y P D P I L L M	
669	AAAAGTGCTAGAAATAGTTGTTGGTCTAAAGATGCAGAATATGGACTCTATTCCATCTAT	728
	-+-----+-----+-----+-----+-----+-----+-----+-----	
224	TTTTACGATCTTTATCAACAACCAGATTTCTACGTCTTATACCTGAGATAAGGTAGATA	243
	K S A R N S C W S K D A E Y G L Y S I Y	
729	CAAGGGGGAATATTTGAGCTTAAGGAAAATGACAGAATTTTTGTTTCTGTAACAAATGAG	788
	-+-----+-----+-----+-----+-----+-----+-----+-----	
244	GTTCCCTTATAAACTCGAATTCCTTTTACTGTCTTAAAAACAAAGACATTGTTTACTC	263
	Q G G I F E L K E N D R I F V S V T N E	
789	CACTTGATAGACATGGACCATGAAGCCAGTTTTTTTCGGGGCCTTTTTAGTTGGCTAACTG	848
	-+-----+-----+-----+-----+-----+-----+-----+-----	
264	GTGAAGTATCTGTACCTGGTACTTCGGTCAAAAAAGCCCCGGAAAAATCAACCGATTGAC	281
	H L I D M D H E A S F F G A F L V G	
849	ACCTGGAAAGAAAAAGCAATAACCTCAAAGTGACTATTTCAGTTTTTCAGGATGATACACTA	908
	-+-----+-----+-----+-----+-----+-----+-----+-----	
	TGGACCTTTCTTTTTCGTTATTGGAGTTTCACTGATAAGTCAAAAGTCCTACTATGTGAT	
909	TGAAGATGTTTCAAAAAATCTGACCAAAACAAACAAACAGAAAACAGAAAACAAAAAAC	968
	-+-----+-----+-----+-----+-----+-----+-----+-----	
	ACTTCTACAAAGTTTTTTAGACTGGTTTTGTTTGTCTTTTGTCTTTTGTTTTTTTTG	
969	CTCTATGCAATCTGAGTAGAGCAGCCACAACCAAAAAATTCTACAACACACACTGTTCTG	1028
	-+-----+-----+-----+-----+-----+-----+-----+-----	
	GAGATACGTTAGACTCATCTCGTCGGTGTGGTTTTTTAAGATGTTGTGTGTGACAAGAC	
1029	AAAGTGACTCACTTATCCCAAGAAAATGAAATTGCTGAAAGATCTTTCAGGACTCTACCT	1088
	-+-----+-----+-----+-----+-----+-----+-----+-----	
	TTTCACTGAGTGAATAGGGTTCTTTTACTTTAACGACTTTCTAGAAAGTCCTGAGATGGA	
1089	CATATCAGTTTGTAGCAGAAATCTAGAAGACTGTCAGCTTCCAAACATTAATGCAATGG	1148
	-+-----+-----+-----+-----+-----+-----+-----+-----	
	GTATAGTCAAACGATCGTCTTTAGATCTTCTGACAGTCGAAGGTTTGAATTACGTTACC	

FIG.1B

1149	TTAACATCTTCTGTCTTTATAATCTACTCCTTGTAAGACTGTAGAAGAAAGCGCAACAA -+-----+-----+-----+-----+-----+-----+-----+-----	1208
	AATTGTAGAAGACAGAAATATTAGATGAGGAACATTTCTGACATCTTCTTTTCGCGTTGTT	
1209	TCCATCTCTCAAGTAGTGTATCACAGTAGTAGCCTCCAGGTTTCCTTAAGGGACAACATC -+-----+-----+-----+-----+-----+-----+-----+-----	1268
	AGGTAGAGAGTTCATCACATAGTGTATCATCGGAGGTCCAAAGGAATTCCTGTTGTAG	
1269	CTTAAGTCAAAAGAGAGAAGAGGCACCACTAAAAGATCGCAGTTTGCCTGGTGCAGTGGC -+-----+-----+-----+-----+-----+-----+-----+-----	1328
	GAATTCAGTTTTCTCTTCTCCGTGGTGATTTTCTAGCGTCAAACGGACCACGTCACCG	
1329	TCACACCTGTAATCCCAACATTTTGGGAACCCAAGGTGGGTAGATCACGAGATCAAGAGA -+-----+-----+-----+-----+-----+-----+-----+-----	1388
	AGTGTGGACATTAGGGTTGTAAACCCCTTGGGTTCCACCCATCTAGTGCTCTAGTTCTCT	
1389	TCAAGACCATAGTGACCAACATAGTGAAACCCCATCTCTACTGAAAGTGCAAAAATTAGC -+-----+-----+-----+-----+-----+-----+-----+-----	1448
	AGTTCTGGTATCACTGGTTGTATCACTTTGGGGTAGAGATGACTTTCACGTTTTTAATCG	
1449	TGGGTGTGTTGGCACATGCCTGTAGTCCCAGCTACTTGAGAGGCTGAGGCAGGAGAATCG -+-----+-----+-----+-----+-----+-----+-----+-----	1508
	ACCCACACAACCGTGTACGGACATCAGGGTCGATGAACTCTCCGACTCCGTCCTCTTAGC	
1509	TTTGAACCCGGGAGGCAGAGGTTGCAGTGTGGTGAGATCATGCCACTACACTCCAGCCTG -+-----+-----+-----+-----+-----+-----+-----+-----	1568
	AAACTTGGGCCCTCCGTCTCCAACGTCACACCACTCTAGTACGGTGATGTGAGGTCGGAC	
1569	GCGACAGAGCGAGACTTGGTTTC -+-----+-----+-----+-----+-----+-----+-----+-----	1591
	CGCTGTCTCGCTCTGAACCAAAG	

FIG.1C

Alignment of AIM-I to Human Fas Ligand
(Similarity = 48.594 % Identity = 22.892 %)

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4 MEVQGGPSLGQTCVLIVIFTVL.....LQSLCVAVTYV 36
  :: ..... | : | .....
15 vdssasspwappgtvpcptsvprpgrpppppppppppppppppppp 64
37 YFTNELKQMQDKYSKSGIACFLKEDDSYWDPNDEESMNSPCWQVKWQLRQ 86
  :. |.....|. |:: | :. :. :|: :|..
65 plp..lpplkkrgnhstglcllvm..ffmvlvalvglglgmfgl.fh|qk 109
87 LVRKMILRTSEETISTVQEKQQNISPLVRERGPQRVAAHITGTRGRSNTL 136
  :. :. :||: ... ||| . . . |: . |. ||:| |::|..
110 elaelrestsqmhtasslekqighpspppekkelrkvahlt...gksnsr 156
137 SSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKGFYYIYS 186
  | | ..... | :||.....|:||||:|. |:|:|
157 smplewedty.....givilsgvkykkgg|vinetglyfvys 193
187 QTYFRFQEEIKENTKNDKQMVQYIYKYTS.YPDPILLMKSAARNSCWSKDA 235
  ..||| :.. |: : : :|.. | ||:|:|:|. : | : ..
194 kvyfr.....gqscnnlplshkvymrnsrypqdlvmmegkmmstcttgq 237
236 EYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLV 280
  :: | | |::|:|...|::|. |: |:::.....| | : :
238 mwar.ssy|gavfn|tsadhlyvnnvsel|vnfeesqtffglykl 281

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FIG.2

Alignment Report of AIM-1, hFas Ligand, TNF- α and TNF- β
by Clustal Method with PAM250 Residue Weight Table

		10	20	30	
1	M	A M M E V Q G G P S L - - - - - G Q T C V L I V I F T V L	AIM 1		
1	M	Q Q P M N Y P C P Q I F W V D S S A T S S W A P P G S V F	FAS LIGAND		
1	M	- - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -	tnfa.pep		
1	M	- - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -	tnfb.pep		
		40	50	60	
26	L	Q S L C V A V T Y V Y F T N E L K Q M Q D K Y S K S G I A	AIM 1		
31	P	C P S C G P R G - - - - - P D Q R R P P P P P P V S P L P	FAS LIGAND		
2	-	- - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -	tnfa.pep		
9	L	P R V C G T T - - - - - - - - - - - - - - - - - - - - - - - - - -	tnfb.pep		
		70	80	90	
56	C	F L K E D D S Y W D P N D E E S M N S P C W Q V K W Q L R	AIM 1		
57	-	- P S Q P L P L P L T P L K K K D H N T N L W L P V V	FAS LIGAND		
12	-	- L A E E A L P - - - - - - - - - - - - - - - - - - - - - - - - - -	tnfa.pep		
17	-	- - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -	tnfb.pep		
		100	110	120	
86	Q	L V R K M I L R T S E E T I S T V Q E K Q Q N I S P L V R	AIM 1		
85	F	F M V L V A L V G M G L G - M Y Q L F H L Q K E L A E L R	FAS LIGAND		
32	F	L S L F S F L I V A G A T T L F C L L H F G V I G P Q R E	tnfa.pep		
21	L	L G L L L V L - - - - - - - - - - - - - - - - - - - - - - - - - -	tnfb.pep		
		130	140	150	
116	E	K G P Q R V A A H I T G T R G R S N T L S S P N S K N E K	AIM 1		
114	E	F T - N Q S L K V S S F E K Q I A N P S T P S E K K E P R	FAS LIGAND		
62	E	S P R D L S L I S P L A Q A V R S S S R T P S D - - - - K	tnfa.pep		
34	G	L P - G V G L T P S A A Q T A R Q H P K M H L A H S T L K	tnfb.pep		
		160	170	180	
146	A	L G R K I N S - - - - - - - - - - - - - - - - - - - - - - - - - -	AIM 1		
143	S	V A H L T G N P H S R S I P L E W E D T Y G T A L I - S G	FAS LIGAND		
88	P	V A H V V A N P Q A E G Q - L Q W L N R R A N A L L A N G	tnfa.pep		
63	P	A A H L I G D P - S K Q N S L L W R A N T D R A F L Q D C	tnfb.pep		

FIG.3A

	190	200	210	
167	L H L R N G K L V I H E K G F Y Y I Y S Q T Y F R F Q E E I	AIM 1		
172	V K Y K K G G L V I N E T G L Y F V Y S K V Y F R G Q S C N	FAS LIGAND		
117	V E L R D N Q L V V P S E G L Y L I Y S Q V L F K G Q S C -	tnfa.pep		
92	F S L S N N S L L V P T S G I Y F V Y S Q V V F S C K A Y S	tnfb.pep		
	220	230	240	
197	K E N T K N D K Q M V Q Y I Y K Y T S - Y P D P I L L M K S	AIM 1		
202	N Q P - - - - - L N H K V Y M R N S K Y P E D L V L M E E	FAS LIGAND		
146	- - - P S T H V L L T H T I S R I A V S Y Q T K V N L L S A	tnfa.pep		
122	P K A P S S P L Y L A H E V Q L F S S Q Y P F H V P L L S S	tnfb.pep		
	250	260	270	
226	A R N S C W S K D A E Y G L - - - - - Y S I Y Q G G I F E L	AIM 1		
226	K R L N Y C - - - - - T T G Q I W A H S S Y L G A V F N L	FAS LIGAND		
173	I K S P C Q R E T P E G A E A K P W Y E P I Y L G C V F Q L	tnfa.pep		
152	Q K M V Y P - - - - - G L Q E P W L H S M Y H G A A F Q L	tnfb.pep		
	280	290	300	
251	K E N D R I F V S V T N E H L I D K D H E A S - F F G A F L	AIM 1		
250	T S A D H L Y V N I S Q L S L I N F E E S - K T F F G L Y -	FAS LIGAND		
203	E K G D R L S A E I N R P D Y L D F A E S G Q V Y F G I I -	tnfa.pep		
176	T Q G D Q L S T R T D G I P H L V L S P S - T V F F G A F -	tnfb.pep		
280	V G -	AIM 1		
278	- K L	FAS LIGAND		
232	- A L	tnfa.pep		
204	- A L	tnfb.pep		

Decoration 'Decoration #1': Box residues that match the
Consensus within 2 distance units.

FIG.3B

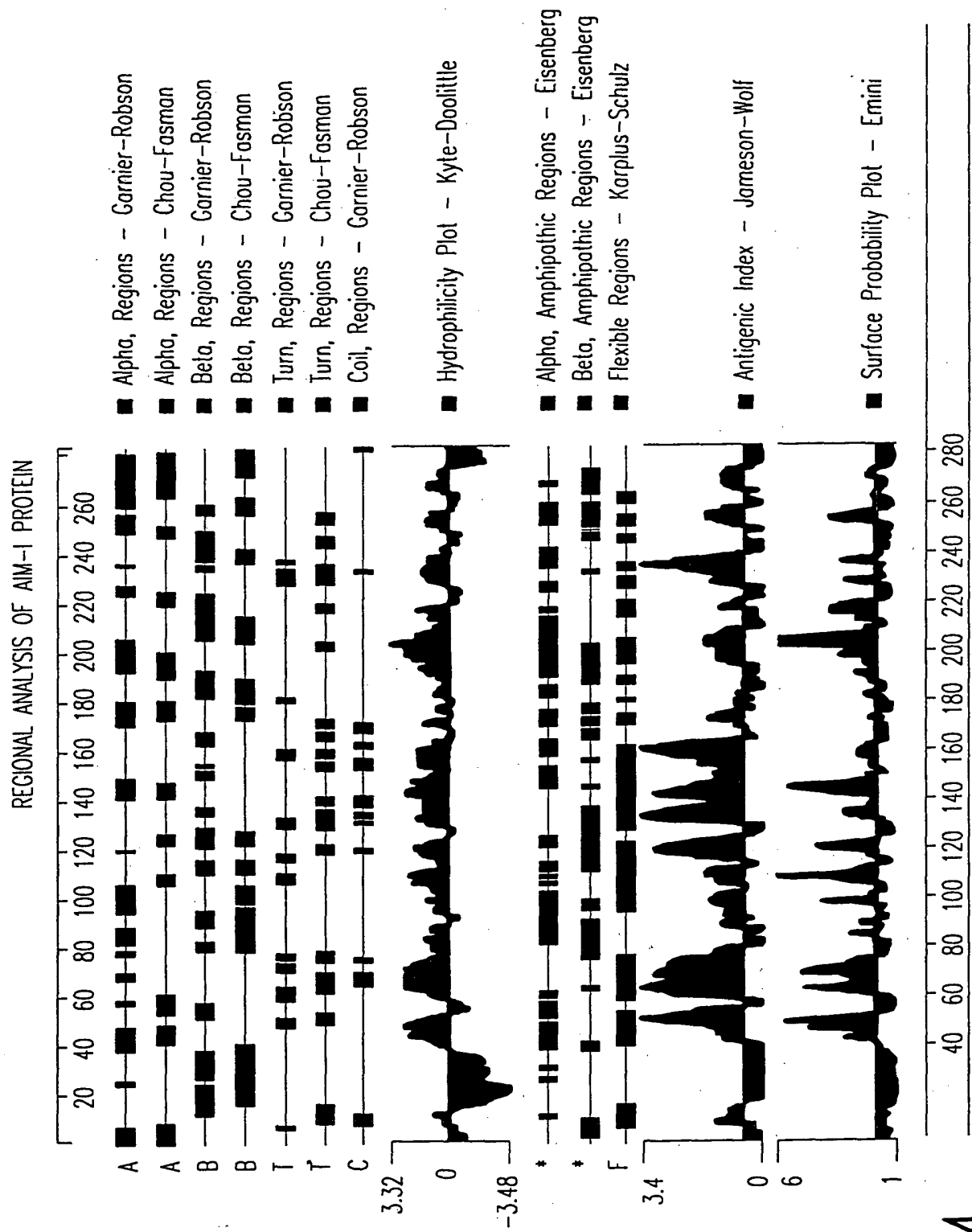


FIG.4